

Resource Summary Report

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Bgee: dataBase for Gene Expression Evolution

RRID:SCR_002028

Type: Tool

Proper Citation

Bgee: dataBase for Gene Expression Evolution (RRID:SCR_002028)

Resource Information

URL: <https://www.bgee.org/>

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Description: Database to retrieve and compare gene expression patterns between animal species. Bgee first maps heterogeneous expression data (currently bulk RNA-Seq, scRNA-Seq, Affymetrix, in situ hybridization, and EST data) to anatomy and development of different species. Bgee is based exclusively on curated healthy wild-type expression data (e.g., no gene knock-out, no treatment, no disease), to provide a comparable reference of gene expression.

Abbreviations: Bgee

Synonyms: Bgee: dataBase Gene Expression Evolution, dataBase Gene Expression Evolution

Resource Type: data or information resource, database

Keywords: gene expression, scrna-seq, rna-seq, affymetrix, in situ hybridization, expressed sequence tag, cross specie, comparison, homology, anatomy, developmental stage, gene expression pattern, development, genome, function, chordate, fish, transcriptome, embryo, adult, mirna, protein coding, prenatal, immature, post-embryonic development, alimentary system, cardiovascular system, nervous system, renal system, reproductive system, respiratory system, skeletal system, ortholog, ontology, FASEB list

Availability: Free, Freely available

Resource Name: Bgee: dataBase for Gene Expression Evolution

Resource ID: SCR_002028

Alternate IDs: nif-0000-11819, r3d100014596

Alternate URLs: <https://doi.org/10.17616/R31NJNR8>

License: CC0

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260905T133115+0000

Ratings and Alerts

No rating or validation information has been found for Bgee: dataBase for Gene Expression Evolution.

No alerts have been found for Bgee: dataBase for Gene Expression Evolution.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 70 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Li S, et al. (2026) Identification of a Diagnostic Gene Signature Associated with Centrosome Amplification in Pressure Injuries: A Cross-Sectional Transcriptome and Machine Learning Study. Journal of inflammation research, 19, 580289.

Ivershina A, et al. (2026) Integrated Analysis of Testicular Histology, Sperm Quality, and Gene Expression (TGFB2, DMRT1) in Rooster Semen (Gallus gallus domesticus). Animals : an open access journal from MDPI, 16(2).

Oishi K, et al. (2026) The Three Pillars of ATP Production in Mammalian Sperm: Integrating Gluconeogenesis Into the Metabolic Framework. Reproductive medicine and biology, 25(1), e70017.

Lamb JW, et al. (2026) Sensory and developmental phenotyping of C. elegans parses autism associated genes into behavioural classifications. bioRxiv : the preprint server for biology.

Bischof F, et al. (2026) Comparative analysis reveals molecular adaptation of mammalian HCA2 to microbial metabolites. iScience, 29(6), 116030.

Zhou X, et al. (2025) Role of the human cytochrome b561 family in iron metabolism and tumors (Review). Oncology letters, 29(3), 111.

Tackie E, et al. (2025) Whole Exome Sequencing Uncovers Genetic Syndromes Associated with Orofacial Clefts presenting with Limb abnormalities in a Sub-Saharan African cohort. Research square.

Bastian FB, et al. (2025) Bgee in 2024: focus on curated single-cell RNA-seq datasets, and query tools. *Nucleic acids research*, 53(D1), D878.

Kaur H, et al. (2024) A pilot study on the differential urine proteomic profile of subjects with community-acquired acute kidney injury who recover versus those who do not recover completely at 4 months after hospital discharge. *Frontiers in medicine*, 11, 1412561.

Sartorius AM, et al. (2024) An evolutionary timeline of the oxytocin signaling pathway. *Communications biology*, 7(1), 471.

Wu Z, et al. (2024) Tumor Heterogeneity of STEAP4 in Malignant Progression of Oral Squamous Cell Carcinoma. *Journal of Cancer*, 15(20), 6754.

Nakamura M, et al. (2024) Unraveling the DNA methylation landscape in dog blood across breeds. *BMC genomics*, 25(1), 1089.

Jankovičová J, et al. (2024) The extracellular vesicle tetraspanin CD63 journey from the testis through the epididymis to mature bull sperm. *Scientific reports*, 14(1), 29449.

Mehta K, et al. (2024) Predictions of Bedaquiline Central Nervous System Exposure in Patients with Tuberculosis Meningitis Using Physiologically based Pharmacokinetic Modeling. *Clinical pharmacokinetics*, 63(5), 657.

Majewska AM, et al. (2024) Secreted novel AID/APOBEC-like deaminase 1 (SNAD1) - a new important player in fish immunology. *Frontiers in immunology*, 15, 1340273.

Goo BS, et al. (2023) Schizophrenia-associated Mitotic Arrest Deficient-1 (MAD1) regulates the polarity of migrating neurons in the developing neocortex. *Molecular psychiatry*, 28(2), 856.

Jankovičová J, et al. (2023) Distribution of tetraspanins in bovine ovarian tissue and fresh/vitrified oocytes. *Histochemistry and cell biology*, 159(2), 163.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. *PloS one*, 18(2), e0279597.

Liang XZ, et al. (2023) IRF8 and its related molecules as potential diagnostic biomarkers or therapeutic candidates and immune cell infiltration characteristics in steroid-induced osteonecrosis of the femoral head. *Journal of orthopaedic surgery and research*, 18(1), 27.

Pedroni L, et al. (2023) A Computational Inter-Species Study on Safrole Phase I Metabolism-Dependent Bioactivation: A Mechanistic Insight into the Study of Possible Differences among Species. *Toxins*, 15(2).